

```
FT      /note= "putative"
```

CKR-2, a human membrane protein that binds to the disordered domain of the type 1 receptor protein tyrosine kinase. Human protein sequence alignment with the partial sequence of the human *trkA* protein. Human *trkB* receptor protein tyrosine kinase. Human *trkB* fusion used in Neurotrophin-3 receptor activation assay. Human *trkC* receptor protein tyrosine kinase. Human *trkC* fusion used in Neurotrophin-3 receptor activation assay. Human *trkA* protein tyrosine kinase. Human *trk* receptor protein tyrosine kinase. Human *trkA* fusion used in Neurotrophin-3 receptor activation assay. Human *trkC* receptor protein tyrosine kinase. Porcine *trkC* protein tyrosine kinase. Human *trkC* receptor protein tyrosine kinase. Human *trkC* receptor protein tyrosine kinase. Adult porcine *trkC* protein tyrosine kinase. *trkC* gene product. Novel human diagnosis of a novel human *trkC* protein. Mouse *trkC* proto-oncogene. Partial *trkC* gene sequence. Murine *TrkC* protein tyrosine kinase. Human protein kinase. Porcine *TrkC* K2 isoform. Murine *TrkC* K3 isoform. Rat muscle-specific tyrosine kinase. Rat *Dmk* receptor protein tyrosine kinase. *Nsk2* receptor with tyrosine kinase activity. Mouse receptor tyrosine kinase. Mouse muscle-specific tyrosine kinase. Mouse *Nsk2* receptor protein tyrosine kinase.

XX 26-NOV-1995 (first entry)

XX Human mammary carcinoma kinase 10 (MCK-10).

DE Mammary carcinoma kinase 10; transmembrane receptor;

KW receptor tyrosine kinase; cancer.

XX Homo sapiens.

XX

Key Location/Qualifiers

FT Peptide 1..18

FT /label= signal

FT Domain 31..185

FT /label= disordered I-like domain

FT Cleavage-site 304..307

FT /label= putative precursor cleavage site

FT Region 417..439

FT /label= transmembrane

FT MISC-difference 505..541

FT /label= alternatively spliced sequence I

FT MISC-difference 666..671

FT /label= alternatively spliced sequence II

FT MISC-difference 25..42

FT /label= NT alpha

FT /note= "peptide antibody recognition site"

FT MISC-difference 309..321

FT /label= NT beta

FT /note= "see above"

FT MISC-difference 909..919

FT /label= CT beta

FT /note= "see above"

PN W09514088-A.

XX 26-MAY-1995.

XX 16-NOV-1994; 94WO-EP03797.

XX 16-NOV-1993; 93US-0153397.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Alves FHE, Ulrich A;

XX MPI; 1995-224054/29.

DR N-PSDB; AA092520.

XX

PT New nucleic acid encoding MCK-10 receptor tyrosine kinase - and

PT derived vectors, transformed cells, proteins and antibodies useful

PT for diagnosis and treatment of proliferative disease, esp. cancer,

PT and for screening modulators

XX

PS Disclosure; Page 53-55; 115pp; English.

XX

CC cDNA prep. from human breast cancer cell line MCF7 (ATCC HTB22) and

CC used in a PCR with two degenerate oligo primer pools based on

CC conserved sequences of the kinase domain of receptor tyrosine

CC kinases. One clone, designated MCK-10, was identified as novel RTK.

CC The PCR fragment was used to screen a lambda gt11 library of human

CC fetal brain cDNA. Several overlapping clones were identified. The

CC composite of these cDNA clones is given in AA092520 and the deduced AA

CC sequence in AA075502. Some of the clones had a deletion of 6 AAs at

CC position 2315 in the MCK-10 sequence. MCK-10 has all the

CC characteristics of a receptor PK (see AA075502 FT). Screening of

CC human placental library yielded two cDNA clones MCK-10-1 and

CC MCK-10-2. One of the clones isolated from the human fetal brain

CC library contd. an additional 18 nts in the TK domain. The MCK-10 splice

CC isoforms have been designated MCK-10-1 (with an additional 111 bp

CC between nts 1832 and 1943); MCK-10-2 (without any insertions); MCK-10-3

CC (with the additional 111 bp and and 18 bp in the TK domain); and MCK10-4

CC (with the additional 18 bp). The predicted mol. wts. of MCK-10-1 and

CC MCK-10-2 proteopreors are 101.13 and 97.17 kD respectively, and can thus

CC be subdivided into a 34.31 kD alpha subunit and and 66.84 or 62.88 kD

CC beta subunits that contain the TK homology and alternative splice sites.

XX

XX Sequence 919 AA:

Query Match 99.9%; Score 4921; DB 16; Length 919;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGEPAISLLILLIVASGADMKGHPAKCYALGMODRTIPDSISSSSSSSTAR 60

DB 1 mgepaissllillivasgadmkghdpakcyaigmqdrtlpsdissasssdstar 60

QY HSRLESSDGDGAWCPAGSVFPEEETLYQVLDRLHLVALYGTGNAGGLKEFSRYRL 120

DB hsrlessdgdgawcpagsvfpkeeylqvdlgrhlhvalvgqgnhagglkfeirsyrl 120

QY 121 RTRSDGRMMGKDRMGQEVISGNEDEPGVVLKDLGPPVAVRLVRFPRADRVMSCLRV 180

DB 121 rtrsdgrmmgkdrmgqevisgnedepgvvlkdlgppmvavrlvrfpradrvmsvclrv 180

QY 181 ELYGCLMRDGLSYAPVQGTMYLSEAYVLYNSTDGHVYGGLOYGGLADYVGLDD 240

DB 181 elygclmrldglstyapvqgtmylseayvlynstdghvyyggloyggladyyvgldd 240

QY 241 FRKSOELRWPGDYVYGVMSNHSFSSGYVMEPEFRLRFAOMQVHCNMHTLGARLGG 300

DB 241 frksaelrwpgdyvygvmsnhsfssgyvmepefrrlrafomqvchcmhtlgarlpgg 300

QY 301 VECRRRRGPMAMEEPMRHNIGNLGDPARAVSVPLGGRVARELQCRFLFAGPMLFS 360

DB 301 vecrrrrgpmameeepmrhnlgnlgdparavsvplggrvarelfqcrflfagpmlfs 360

QY 361 EISFISDVYNNSSPALGFFPPAPPMWPPGPPPTNSSLELFRGQOPPAKAGSTALLI 420

DB 361 eisfidvyvnnsspalgffppapppmwppppptnsslelfrgqoppakagstalll 420

QY 421 GCLVAIIILLIILMLRLMRLMRLLSKAERVLEETLVLSVPGDTIILNNPGRRE 480

DB 421 gclvaliillliilmlrlmrlmrlskaervleeltvlsvpgdtiilnnpgrre 480

QY 481 PPPYDEPRRGNPPHSAPCVNPGSALLSNPARYLLLATYARPPRGPPTPAMAKPNT 540

DB 481 ppydeprrgnpphsapcvnpgsalllnparylllatyarprrgpptpamakpnt 540

QY 541 QAYSQDYMPEKRGAPRLPPPPQNSVPHYAEADYTLQGVYGGNTYVAPALPGAVGDP 600

DB 541 qaysqdympkrgaprlppppqnsvphyaeadytlqgvyygntyvapalpgavgdp 600

QY 601 PRVDPFRRLRFKEKLGEGFGEVHLCEVDSFODVSLDFPLNVRKGGPLLVAKTLRPD 660

DB 601 prvdprrrlrfkeklgsegfgevhlccevdspfodvslfplnvrrkggpllvaktlrpd 660

QY 661 ATKNASFSLFRNDLFKEVKTMSRLKDPNIIRLGVCVQDDPLCWITDYMENGDLNGLFS 720

DB 661 atknasfslfrndlfkevktmsrlkdpniiirlgvcvqddplcmldymengdlnqlfs 720

QY 721 AHOLEDKAKBAPGGGQAAGPTISYPLLVAQAQAGMRYLATLNVRHDLATRNCLV 780

DB 721 aholedkakaagpggqaagptisyppllvaagaqagmrylatlnvrhldatrnclv 780

QY 781 GENTFIKADGMSRNLTAGDYVYRQGAVALPIRMAMECTIMKFTTASDVNAFGYTLW 840

DB 781 gentfikadgmsrnltagdyvyrqgavalpirmamectimkfttassdvnafygtlw 840

QY 841 EYLMKRAQPPGQUTDEQVYNAGPEFRDGRQYLYSRPPACPGGLYELMKRCSRSSEQ 900

DB 841 eylmkraqppgqutdeqvynagpefrdgrqylysrppacpgglyelmkrcsrsseq 900

QY 901 RPPFSOLHRLFAEDALNTV 919

DB 901 rppfsqlhrlfaedalnrv 919

RESULT 3
 ID AAR75504 standard; Protein; 919 AA.
 XX AAR75504;
 XX AAR75504;
 XX 26-NOV-1995 (first entry)
 XX
 XX Human mammary carcinoma kinase 10 (MCK-10).
 XX
 XX Mammary carcinoma kinase 10; MCK-10; transmembrane receptor;
 XX receptor tyrosine kinase; cancer.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..18
 XX Domain /label= signal
 XX /label= discolidin I-like domain
 XX Cleavage-site 304..307
 XX /label= putative precursor cleavage site
 XX Region 417..439
 XX /label= transmembrane
 XX MISC-difference 505..541
 XX /label= alternatively spliced sequence I
 XX MISC-difference 666..671
 XX /label= alternatively spliced sequence II
 XX MISC-difference 25..42
 XX /label= NT alpha
 XX /note= "peptide antibody recognition site"
 XX MISC-difference 309..321
 XX /label= NT beta
 XX /note= "see above"
 XX MISC-difference 909..919
 XX /label= CT beta
 XX /note= "see above"
 XX
 XX W09514089-A.
 XX
 XX 26-MAY-1995.
 XX
 XX 16-NOV-1994; 94MO-EP03799.
 XX
 XX 16-NOV-1993; 93US-0153397.
 XX
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 XX Alves FHE, Ullrich A;
 XX
 XX WPI; 1995-224055/29.
 XX N-PSDB; AA092522.
 XX
 XX New nucleic acid encoding CCK-2 receptor tyrosine kinase - and
 XX derived vectors, transfected cells, proteins and antibodies, useful
 XX for diagnosis and treatment of proliferative and nervous system
 XX diseases and for screening modulators
 XX
 XX Disclosure: Page 70-72; 115pp; English.
 XX
 XX CDNA prep'd. from human breast cancer cell line MCF7 (ATCC HTB22) was
 XX used in a PCR with two degenerate oligo primer pools based on
 XX conserved sequences of the kinase domain of receptor tyrosine
 XX kinases. One clone, designated MCK-10, was identified as novel RTK.
 XX The PCR fragment was used to screen a lambda gIII library of human
 XX fetal brain cDNA. Several overlapping clones were identified. The
 XX composite of these cDNA clones is given in AA092522 and the deduced AA
 XX sequence in AAR75504. Some of the clones had a deletion of 6AA at posn.
 XX 2315 in the MCK-10 sequence. MCK-10 has all the characteristics of
 XX a receptor PTK (see AAR75504 FT). Screening of human placental library
 XX yielded two cDNA clones. One of the clones isolated from the human

CC fetal brain library contained an additional 18 nts in the TK
 CC domain. The MCK-10 splice isoforms have been designated MCK-10-1
 CC (with an additional 111 bp between nts 1832 and 1943); MCK-10-2
 CC (without any insertions); MCK-10-3 (with the additional 111 bps and
 CC 18 bp in the TK domain); and MCK-10-4 (with the additional 11 bp).
 CC The predicted mol. wts. of MCK-10-1 and MCK-10-2 precursors are
 CC 101.13 and 97.17 kD respectively, and can thus be subdivided into a
 CC 34.31 kD alpha subunit and a 66.84 or 62.86 kD beta subunits that
 CC contain the TK homology and alternative splice sites.
 CC
 SQ Sequence 919 AA;
 Query Match 99.98; Score 4921; DB 16; Length 919;
 Best Local Similarity 99.98; Pred. No. 0;
 Matches 918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGPEALSSLLLLLVASGDADMKGFDPKACRYALGMDRTIPSDISASSMSDSTAA 60
 Db 1 mgpealsslllllvassgdadmkgfdpakercryalgmdrtipdsdissasswdsaa 60
 QY 61 HSRLESSDGGACWCPAGSVPFKKEEYIQVDLQRLHLVALVGTGRHAGGLAKESRSYRL 120
 Db 61 hsrlesddggacwcpagsvfpkkeeyiqvdlqrlhlvalvgtgrhagglaketsrsyrl 120
 QY 121 RYSHDGRMMGKMDRMGOEYISGNEDEGVYLKDLGPMYARVRYPRADRVMSYCLRV 180
 Db 121 rysdgrmmgkmdrmgoeyisgndegvylkdlgpmyarvrypradrvmsyclrv 180
 QY 181 ELYGCLMRDGLSYTAVVGOTMYLSEAVYINDSTYDGHFTVGGTGLGGLADGVGLDD 240
 Db 181 elygcclmrddlsytavvgotmylseavyindstydghftvvggtglggladgvvgldd 240
 QY 241 FRKSOELRWVPGDYVMSKHSFSSGYVEKEFEEDRLRAFOAMQVHCNNMHTLCARLPGG 300
 Db 241 frksaelrwvpgdyvmskhsfssgyvekefedrlrafoamqvhcnnmhtlcarlpgg 300
 QY 301 VECFRFRGPAMAWGEPHNRNLGNLGDPRARAVSVPLGGRVAFRLCRLFLPAGPWLIFS 360
 Db 301 vecfrfrgpamawgephnrnlgnlgdpraravsvplggrvafrlcrlflpaggpwlifs 360
 QY 361 EISFISDVVNSSPALGTFPPAPWMPGPPPTNFSSLSLEPRGOQVAKAEGSPYALI 420
 Db 361 eisfisdvvnsspalgtfppapwmpgppptnfsslsleprgoqvakaegspyalil 420
 QY 421 GCLVATILLLLILALMLMLHMRRLSKAERYLEBELTVHLSVPGDTLLINRPGPRE 480
 Db 421 gclvatilLLLILALMLMLHMRRLSKAERYLEBELTVHLSVPGDTLLINRPGPRE 480
 QY 481 PPYQEPFRPGNPNPHSAPCVNPGSALLSNPARYRLILATYARPPRGPPPTPMAKPTNT 540
 Db 481 ppyqepfrpgnpphspcvnpgsallsnparyrlllatyarprrgppptpmaapnt 540
 QY 541 QAYSQGYMEPEKPGAPLPPPPONSVPHYAADIIVTLOGVTGNTYAVPALPPGAVDGP 600
 Db 541 qaysqgyમેpekpgaplpppponsvphyadivtlogvtgntyavpalppgavdgdp 600
 QY 601 PRYDFPRSRRLRFKXKGEQGFGEVHCEVDSPPDLYSLDPLVNRKGNPLVAVKILRPD 660
 Db 601 prydfrsrRLRFKXKGEQGFGEVHCEVDSPPDLYSLDPLVNRKGNPLVAVKILRPD 660
 QY 661 ATKNAFSLSFRNDFLEKVIKMSRLKDPNIRILGVCYODDPCLMTDVENEDLNQOFLS 720
 Db 661 atknafslsfrndflekvikmsrlkdpnirilgvcyoddpclmtdivenedlnqfls 720
 QY 721 AHOLEKAAAGAPDGOAAGPTISYPMLELHVAQAQASGRYLATINFYHRDLATRNCLY 780
 Db 721 aholekaagapdgaaqgptisypmllelhmaaglasgmylatinfhrdlatrncl 780
 QY 781 GENFTTKINDFGMSRLYAGDYRVVGRVAVLPFRMAECILMGKTTASDVAFCVTLM 840
 Db 781 genfttkindfgmsrlyagdyrvvgrvavlpfrmaecilmgkttasdvafcvtlw 840

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QY 841 EYVLMCRAPFGQLTDEQVIENAGEFFRDGROYLSRPPACPOGLYEIMLCWMSRESE 900
DB 841 EVMLICRAQPIGQITDEQVIENAGEFFRDGROYLSRPPACPOGLYEIMLCWMSRESE 900
QY 901 RPPFSQHLRFIAEDALNTV 919
DB 901 RPPFSQHLRFIAEDALNTV 919

RESULT 4
AAR71100
ID AAR71100 standard; Protein; 914 AA.
AC AAR71100;
DT 17-AUG-1995 (first entry)
DE Protein-tyrosine-kinase PTK22.
XX
XX Protein-tyrosine-kinase; PTK; discoidin domain receptor; cancer;
XX breast tumor; mamma carcinoma; diagnosis; prognosis; therapy.
XX
XX Homo sapiens.
XX
XX MO9502187-A.
XX
XX 19-JAN-1995.
XX
XX 08-JUL-1994; 94MO-GB01480.
XX
XX 09-JUL-1993; 93GB-0014271.
XX
XX (CANC-) CANCER RES INST.
XX (WELL) WELLCOME FOUND LTD.
XX
XX Barker KT, Crompton MR, Gusterson BA, Martindale JE;
XX Mitchell PJ, Page MJ, Spence P;
XX
XX WPI: 1995-066991/09.
XX N-PSDB; AA084782.
XX
XX Method for screening substances, using protein tyrosine kinase -
XX for potential utility as therapeutic agents for cancer
XX
XX Disclosure: Page 26-30; 51pp. English.
XX
XX cDNA derived from tumor metastatic tissue was amplified using
XX primers (given in AA084783-84) based on sequences (AAR71101, AAR71103)
XX associated with protein-tyrosine-kinases (PTK). Novel PTK22 was
XX identified in an isolated subclone. The 3' sequence of PTK22 was
XX obtained by reverse transcription (using the primer of AA084786) and
XX PCR amplification (primers AA084787-88) of RNA of human breast
XX carcinoma cell line MDA MG 468. The partial DNA sequence of PTK22
XX is given in AA084782.
XX
XX Sequence 914 AA:

```

```

QY 181 ELYGCLMRBGLLSTAPVGTMTLSEANTYLNDSITDGHVGLGGLGCLADGVGLDD 240
DB 181 ELYGCLMRBGLLSTAPVGTMTLSEANTYLNDSITDGHVGLGGLGCLADGVGLDD 240
QY 241 FRKSOELRWMPGYDVGVNSHSFSSGYEMEEEDRLRAFQAMQVHONMHTLGAARLPG 300
DB 241 FRKSOELRWMPGYDVGVNSHSFSSGYEMEEEDRLRAFQAMQVHONMHTLGAARLPG 300
QY 301 VECRRRGPAMAMGEPMRHNLAGNLGDPARAASVPLGGRVAFRLQCFLEAPWILFS 360
DB 301 VECRRRGPAMAMGEPMRHNLAGNLGDPARAASVPLGGRVAFRLQCFLEAPWILFS 360
QY 361 EISFISDVVNSSPALGCTPPAPWMPGPPTNFSLELEPRGO-OPVAKESGPTAIL 419
DB 361 EISFISDVVNSSPALGCTPPAPWMPGPPTNFSLELEPRGO-OPVAKESGPTAIL 419
QY 420 IGCIVATILLLILIALMLMRLLHRRLLSKARVLEELTVHLSVPGDTLLNNRGP 479
DB 420 IGCIVATILLLILIALMLMRLLHRRLLSKARVLEELTVHLSVPGDTLLNNRGP 479
QY 480 EPPYOEPRRGNPNSAPCVPNCSALLSNPARYRLATYARPRGPGPTPAMAKPTN 539
DB 480 EPPYOEPRRGNPNSAPCVPNCSALLSNPARYRLATYARPRGPGPTPAMAKPTN 539
QY 540 TOAVSGDIEMEPKGPALLPBPQNSVPHVAEADIVTLGGVTGNTYAVPALPGAVDG 599
DB 540 TOAVSGDIEMEPKGPALLPBPQNSVPHVAEADIVTLGGVTGNTYAVPALPGAVDG 599
QY 541 TQAYSQDYMEPEKPGAPLPPPPQNSVPHVAEADIVTLGGVTGNTYAVPALPGAVDG 600
DB 541 TQAYSQDYMEPEKPGAPLPPPPQNSVPHVAEADIVTLGGVTGNTYAVPALPGAVDG 600
QY 600 PPRVDFPRSRRLREKEXIGEFGFVHCEVDSPODDVLSDFPLNVRKGHLVAVKILRP 659
DB 600 PPRVDFPRSRRLREKEXIGEFGFVHCEVDSPODDVLSDFPLNVRKGHLVAVKILRP 659
QY 601 PPRVDFPRSRRLREKEXIGEFGFVHCEVDSPODDVLSDFPLNVRKGHLVAVKILRP 660
DB 601 PPRVDFPRSRRLREKEXIGEFGFVHCEVDSPODDVLSDFPLNVRKGHLVAVKILRP 660
QY 660 DATKNAFSLSFRNDFLEKVKINSRLKDPNIRLLGYCVODDPCLMTDYNENGDLNQFL 719
DB 660 DATKNAFSLSFRNDFLEKVKINSRLKDPNIRLLGYCVODDPCLMTDYNENGDLNQFL 719
QY 720 SAHOLEDKAABGAPDGOAAAGPTISYPMLLHVAQAQIASGMRYLATLNFYHRLAENCL 779
DB 720 SAHOLEDKAABGAPDGOAAAGPTISYPMLLHVAQAQIASGMRYLATLNFYHRLAENCL 779
QY 775 VGENFTIKINDFGSRNLYAGDYRVGKAVLPTRMMAMCILMGKTTASDVWAGVYL 839
DB 775 VGENFTIKINDFGSRNLYAGDYRVGKAVLPTRMMAMCILMGKTTASDVWAGVYL 839
QY 840 WEVLMCRAPFGQLTDEQVIENAGEFFRDGROYLSRPPACPOGLYEIMLCWMSRESE 899
DB 840 WEVLMCRAPFGQLTDEQVIENAGEFFRDGROYLSRPPACPOGLYEIMLCWMSRESE 899
QY 900 QRPFSQHLRFIAEDALNTV 919
DB 900 QRPFSQHLRFIAEDALNTV 919

RESULT 5
AAM34673
ID AAM34673 standard; Protein; 882 AA.
AC AAM34673;
DT 17-FEB-1998 (first entry)
DE Human mammary carcinoma kinase 10 (MCK-10) splice variant 1.
XX Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase;
XX proliferative disease; cancer; insulin receptor family;
XX tyrosine kinase neurotrophin receptor; MCK-10 activity;
XX neurological disorder; aberrant expression.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..18

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RESULT	6
AAW34675	standard; Protein; 876 AA.
AAW34675	
17-FEB-1998	(first entry)
Human mammary carcinoma kinase 10 (MCK-10) splice variant 3.	
Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase; proliferative disease; cancer; insulin receptor family; tyrosine kinase neurotrophin receptor; MCK-10 activity; neurological disorder; aberrant expression.	
Homo sapiens.	
Key	Location/Qualifiers
Peptide	1..18
Protein	/label="signal_sequence
Domain	19..876
Cleavage-site	/note="mature_protein"
Region	31..185
Binding-site	/label="Discoidin_I-like_domain
Modified-site	304..307
Modified-site	/label="endopeptidase_furin
Modified-site	/note="putative precursor cleavage site"
Modified-site	48..439
Modified-site	/label="transmembrane_region
Modified-site	580..590
Modified-site	/label="ATP_binding_motif
Modified-site	760..761
Modified-site	/label="autophosphorylation_sites
Modified-site	/note="putative"
Modified-site	756..756
Modified-site	/label="autophosphorylation_site
Modified-site	/note="putative"
Modified-site	802..805
Modified-site	/label="binding_motif_for_PI3_kinase
Modified-site	/note="binding motif for phosphatidylinositol 3' kinase"
Binding-site	790
Binding-site	/label="potential_substrate_binding_site
Binding-site	26..42
Binding-site	/note="antibody recognition sequence Nalpha"
Binding-site	309..331
Binding-site	/note="antibody recognition sequence Nbeta"
Binding-site	860..877
Binding-site	/note="antibody recognition sequence Cbeta"
US567144-A.	
14-OCT-1997.	
08-NOV-1994;	94US-0336343.
16-NOV-1993;	93US-0153397.
(ALVE/) ALVES F H E.	
(ULR/) ULRICH A.	
Alves FHE, Ulrich A;	
WPI. 1997-511869/47.	
Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding for it, useful for cancer diagnosis	
Disclosure; Page -, 70pp; English.	
The present sequence represents a splice variant of a mammary	

CC carcinoma kinase (MCK-10). This kinase belongs to a novel family
CC of receptor tyrosine kinases, and expression is associated with
CC proliferative diseases such as cancer. The MCK-10 receptor tyrosine
CC kinase has extensive sequence similarity to the insulin receptor family.
CC The MCK-10 gene was isolated by PCR using 2 degenerate oligonucleotide
CC primer pools, using a template cDNA synthesised by reverse transcription
CC of poly(A) RNA from the human mammary carcinoma cell line MCF7. The
CC amplified PCR product was used to screen human foetal brain and
CC placental libraries, from which the present splice variant was isolated.
CC This splice variant does not possess amino acids 505-541 or 666-671 of
CC MCK-10 (AAW345672). The sequence represented by amino acids 548-558 may
CC be important, as deletion of this motif in the activin receptor
CC serine/threonine kinase results in reduced ligand binding affinity.
CC MCK-10 is expressed in brain tissue, and the protein shares homology
CC with the tyrosine kinase neurotrophin receptor. Modulation of MCK-10
CC activity therefore may be used for treatment of neurological disorders.
CC MCK-10 is also expressed in a variety of cancer cell lines and tumour
CC tissue. The nucleotide sequence of MCK-10, or parts of it, can be used
CC for diagnostic purposes to detect aberrant expression of MCK-10 genes.
CC Inhibitors of MCK-10 (or splice variants) receptor activity may have
CC therapeutic value in the treatment of diseases such as cancer.
CC note: the present sequence does not appear in the specification, but was
CC created using information provided.

Query Match	94.58;	Score 4656.5;	DB 18;	Length 876;
Best Local Similarity	95.38;	Pred. No. 0;		
Matches 876; Conservative	0;	Mismatches	0;	Indels 43; Gaps 2

QY	1	MEPELASSLILLLLILVASGDADKMGHFDPAKCYALAGMDORTPBSDIASASSMSNSTAAR	60
Dd	1	mpbealslililililvasgadmkyhldpkckryalgmdqrltpdsdiassswwstear	60
QY	61	HSRLSSDGDGAMCPCAGSVFPKEEERYLQYDLORLHVALVPGOHAGSLGKEFERSYRL	124
Dd	61	harslesddgdgawcpagswfpekeeylqvdqlrhlvalvpgqrhaggjgkefersyrl	124
QY	121	RSRQGRMMKMKDKMWGEVLSGNDDPEGVYLKLDGPPWAKRLVNFYTRADRWSCYLRV	188
Dd	121	rysigrmmgkdkdwggevlsngdpegvylkldgppmwavrlvrfytradrwmsvclrv	188
QY	181	ELYGLMRDGLLSYAPVQGTWYLTSEAVYLYNDSTRDXTGHTVGGLAGGGGQLADGVGDD	244
Dd	181	elyglrwdgllsypapqgctmlylseavylndstrydghtvsgllqyqglagqladgyvgidd	244
QY	241	FRKSELKAWPQGYDYGVGSNNHSFSSGGYEMEFEDRLRAFOAMOVHNNMHTLGARLPFG	300
Dd	241	fkselkltvwpgydygvgsnnhsfssegymefefrlraifamqvchcnmhtlgarlpbg	300
QY	301	VECFRRCPAPAMAEDEEPRHNLGMLGPPRARAAVSPRGGRARPLQCRFLPAGWLLFS	366
Dd	301	vecfrrcpamawegemprhnlgnlpgpraravsprggrarplqcrflfagpwlifs	366
QY	361	EISFISDLYNNSSPALGSTFPAPKWPMPRGPPPTNFSSTLELPRGOQYPAKKEGSPITALI	422
Dd	361	eisfisdvnnsspalgstfpapwmprgppptfisslelprgqvapakegspitali	422
QY	421	GCILVAILLLLLILALMLMRLLMRRLLSKAEPRVLEELTYHLSPVGGTILILNRPGR	488
Dd	421	gclvailililililalmrllmrllmrllskaeprvleeltyhlsvpogtliilnrpgr	488
QY	481	PPPIQEPFRKGNPHRSAPCVNNGSALLISNPAHYRLLLATYARPPRGREPPTPAMAKPTNT	544
Dd	481	pppyqepfrpknphrsapcvnngsallisnpahyrllllatyarpprgreppptpamakptnt	544
QY	541	QAYSGDYMEPRPGAPLILPPRPNOSVPHXADIVTLQGVYGNATYVAPLPRGAYDGP	600
Dd	505	-aysgdympckgparlilpprpqnsvphyaadivtlqgvynatylvraplpprayvgdp	566
QY	601	PRVDFPNRLFKKELGBOGEGEYHLCVDSPODLVSLDRPLNTRKGNHLLVAVKILRPD	666

Db 564 pvdfrprsrllfkeklgeqfgevhlcevdspqdlvaldfplnvkrkphllvavkllrpd 623
QY 661 ATKAAASGSLSRNDPLFEKWKIMSKLPNIRRLIGVCVQDDPLCMITDYMENGDLPFLS 720
Db 624 atkna-----rnfllkevkmrllkqpnllrlllgvcvqddplcmldymengdlngfls 677
QY 721 AHOEDKRAEGAPDGGAAAGPTISYPMLLHVAQAISGMRXYLATLNFVRHDLATRNCLV 780
Db 678 ahqledaaagapdggaagqptlsypmllhvaaglasgmtyatlfnvrdlatrncly 737
QY 781 GENTTIKADFGMSRNLVAGDYRVQGRAVLPFRMAAMECTIMGKFTTASDVMAFVTLW 840
Db 738 genttikadfgmsernlvagdyyrvqgravlpfrmaamecclngkfttasdvaafvltw 797
QY 841 EYLMCLRAQPFQQLTDBQVIENAGEFFRDGROYLTSRPACPGYLEMLRCWSRESEQ 900
Db 798 evlmclraqpfqqltdeqvienegeffrdgroyltsrppacpglyelmrcwsresed 857
QY 901 RPPSOHLRFLAEDALNTV 919
Db 858 rppstqlhrflaedalnvt 876

RESULT 7
AAB54286
ID AAB54286 standard; Protein: 624 AA.
AC AAB54286;
DT 09-MAR-2001 (first entry)

Human pancreatic cancer antigen protein sequence SEQ ID NO:738.
XX
KW Human; Pancreas; pancreatic cancer; pancreatic cancer antigen;
KW detection; diagnosis; identification; cytostatic; neuroprotective;
KW neurotropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW antineoplastic; cardiant; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic;
KW neural; immune system; muscular; reproductive; gastrointestinal;
KW pulmonary; cardiovascular; renal; proliferative.
XX
OS Homo sapiens.
XX
PN WO200055320-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000MO-US05989.
XX
PR 12-MAR-1999; 9905-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-579444/54.
XX
DR N-PSDB; AAC99051.
XX
PT New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition -
PS Claim 11; Page 1180-1182; 1379pp; English.

AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,
CC neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,
CC gynaecological, cardiant and antiinflammatory activities, and can be used
CC in gene therapy. The polynucleotide and proteins can be used for
CC preventing, treating, or ameliorating a medical condition or in assays
CC for diagnosing a pathological condition or a susceptibility to one in a
CC subject. Binding partners to the proteins and the activity of the

CC proteins can be identified. The pancreatic cancer antigens can be used to
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be used to design nucleic
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC analysis, tissue identification and/or typing and a variety of forensic
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 624 AA;

Query Match 66.9%; Score 3298; DB 21; Length 624;
Best Local Similarity 98.7%; Pred. No. 7.7e-245;
Matches 616; Conservative 0; Mismatches 2; Indels 6; Gaps 1;

QY 261 HSPSSGYVEMEEFERDLRAQAMOVHONNHTGLARLPGVCEFRRGPAWAGEPRRH 320
Db 3 hstssgyvemefeirlrafqamqvhcnmhtlgarlpgvcefrirgpanawageprmh 62
QY 321 NLGSLDPPARAAYVPLGGRVAFRLQCRFLFAGPWLFEISFISDVVNSSPALGTF 380
Db 63 nlgsnldppararavsvplggrvarflqcrflfagpwlffesfistdvvnsspalgltf 122
QY 381 PPAPWMPGPPPTNFSSLELEPRGQAPVAKAEGSPALIGLVAIILLLLITALLMLWR 440
Db 123 ppapwmpgppptnfssleleprgqpvaeksgspalilgclvaliilllllitalmlwr 182
QY 441 LHMRLSLKAEKRYLEELVHLSVPGDTLLINRPGPREPPRQGERRGNPHSPCV 500
Db 183 lhmrlslkxerlyleelvhlsvpgdtllinrpprepprpyqeprrpynphspsc 242
QY 501 PNGSALLSNPARYLLATYARPRGPGPTPAMAKPTNTQAYSGDYMEPEKPAAPLPP 560
Db 243 pngsaallsnpaylllatyarpprgpprpapwaklnqaysgdyમેપેકપાપલ 302
QY 561 PPNQSVPHYAEADIVTLQGYTGCTAVVPALPGAVDGPDPVPPSRLLFEKLCBGQ 620
Db 303 ppnqsvphyaeadivtlqgytgntlyavpalpgavdgpprvdfrsrllfkeklgeq 362
QY 621 FGEVHLCEVDSPODLVLDPLNVRKGPPLLVAVKIIRPATKAAASLSLRNPLFEVK 680
Db 363 fgevhlcevdspqdlvaldfplnvkrkphllvavkllrpdackna-----rnfllkev 416
QY 681 IMSRKDPNIRRLIGVCVQDDPLCMITDYMENGDLPFLSAHOEDKRAEGAPDGGAAQ 740
Db 417 imsrkdpnllrlllgvcvqddplcmldymengdlngflsaahqledaaagapdggaq 476
QY 741 GPITISYPMLLHVAQAISGMRXYLATLNFVRHDLATRNCLVGENFTTIADFGMSRNLVAG 800
Db 477 gptisypmllhvaaglasgmtyatlfnvrdlatrnclygenttikadfgmsernlv 536
QY 801 DYRVQGRAVLPFRMAAMECTIMGKFTTASDVMAFVTLWELMCLRAQPFQQLTDBQVI 860
Db 537 dyrvqgravlpfrmaamecclngkfttasdvaafvltwelmclraqpfqqltdeqvi 596
QY 861 ENAGEFFRDGROYLTSRPACPG 884
Db 597 enageffrdgroyltsrppacpg 620

RESULT 8
AAG73767
ID AAG73767 standard; Protein: 624 AA.
AC AAG73767;
DT 03-SEP-2001 (first entry)

DE Human colon cancer antigen protein SEQ ID NO:4531.
 XX
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; chromosome 6.
 XX
 OS Homo sapiens.
 XX
 PN WO200122920-A2.
 PD
 XX 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-US26524.
 XX
 PR 29-SEP-1999; 99US-0157137
 PR 03-NOV-1999; 99US-0163280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX
 PI MPI: 2001-235357/24.
 DR N-PSDB; AAH33198.
 XX
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PR useful for preventing, diagnosing and/or treating colorectal cancers -
 PS
 XX
 PS Claim 11; Page 6327-6329; 9803pp; English.
 XX
 CC AAH32943 to AAH37195 and AAC73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patients own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated P,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P may be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC present invention.
 CC
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 XX Sequence 624 AA:

Query Match	66.9%	Score 3298	DB 23	Length 624
Best Local Similarity	98.7%	Pred. No. 7.7e+24		
Matches	616	Conservative	0	Mismatches 2
			Indels	6
			Gaps	1
QY	261	HSFSSGYEMEFEDRLRAFMQVHCNNMHTLGLARLPGVCERFRRCGPAMAEGERPMR	320	
Db	3	hsfssgyemefefarlafqamqchcmhlllgarlpgvcecfrrgpmawegpmh	62	
QY	321	NLGGNLGPPRRARAVVPILGGVRAFLQCRFLFAGMILLFSEISFISDVNNSSPALGCF	380	
Db	63	nlgnglqpprraravsvplggvraarflqcrflfagpmlfseisfisdvnnsspalggrt	122	
QY	381	PPAPMPGPPPTNFSLELEBRGQOPVAKAEGSPAILIGCLVAIIILLDITLMTMR	440	
Db	123	ppapmpgppptnfsisleprgqpvakegspstailigclvailllllllamlmr	182	
QY	441	LHWRLRLKAERRLVEEETVHLISVGGTIIINNPGREPPPYCEPRGNGPSPAPCV	500	
Db	183	lhwrrlxlkxerivleeeetvhlisvpgdtllinnpgrepppyepirpnpplisapcv	242	
QY	501	PNGSALLISNPAIRLLLATVARRPPRGPGPPPPAMAKPTNTQVAGSDYMEPEKRGAPLLPP	560	

ID	Accession	Standard	Protein	Residue
Db	243	pnsgsallsnpeayrlllllatyarprrpqprrcpawakrntqagdydmepekpgaprlpp		302
Qy	561	PNQSNVPHNAEADYITLQGYMGNGNYANPALPPAVGSGPPRPDPSPSRLEFKKLEEG		620
Db	303	pqnasvphyaeadlytllqgvvgngelyavpalppgavgdpprvdiprsrlrfkeklyeqg		362
Qy	621	FGEVHLCEVDSQODVLSIDFPLNVKGGAPLLVAVKILRPDATTNASSPSLSRNDFLKEV		680
Db	363	fgevhlcevdspqdlvsyldfprlnvzkgprrllvaekllrpdatkna-----ndfllevk		416
Qy	681	INSRLKDPNIIRLGLVCVQDDPLCMITDYMENGDLNQLSAHQLEDKRAEGAPDGGAAQ		740
Db	417	lnsrllkdpnllrlllgvcvgddplcmldtymengdlnqlsahqledkaegapddgaaq		476
Qy	741	GPTISPMILHYAAQILASGMRYALNLNVHDLATRNQLVGEENTTIRIADPGMSRNLYAG		800
Db	477	gptispmllhyaaqilasgmryalaInlvhldatrnqlvgeentfllklnadfgmsrnlYag		536
Qy	801	DYRYVQGRAVPIPIRMNAECCILMGKFTTASDYMAFGVLYMEVLMACRAQPFGLTDEQV		860
Db	537	dyryvgravrlpirmnawecilmgkfttasdsyvaifgyrlwvrlncraqpfqgltdeqvl		596
Qy	861	ENAGEFPFDQGRQVYLSRPPACQ 884		
Db	597	enageftrdqgrvylsrppacq 620		
RESULT 9				
AAW34674	ID	AAW34674	standard; Protein; 563 AA.	
XX	XX	AAW34674;		
XX	DT	17-FEB-1998	(first entry)	
DE	XX	Human mammary carcinoma kinase 10 (MCK-10) splice variant 2.		
XX	XX			
KW	KW	Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase;		
KW	KW	proliferative disease; cancer; insulin receptor family;		
KW	KW	tyrosine kinase neurotrophin receptor; MCK-10 activity;		
XX	XX	neurological disorder; aberrant expression.		
OS	XX	Homo sapiens.		
FH	FH	Key	Location/Qualifiers	
FT	FT	Peptide	1..18	
FT	FT	Protein	/label= signal_sequence	
FT	FT	Domain	19..919	
FT	FT	Cleavage-site	/note= "mature_protein"	
FT	FT	Region	31..185	
FT	FT	Modified-site	/label= DiscoIdin_I-like_domain	
FT	FT	Region	304..307	
FT	FT	Modified-site	/label= endopeptidase_furin	
FT	FT	Region	48..439	
FT	FT	Modified-site	/note= "putative precursor cleavage site"	
FT	FT	Region	617..627	
FT	FT	Modified-site	/label= transmembrane_region	
FT	FT	Region	617..627	
FT	FT	Modified-site	/label= ATP_binding_motif	
FT	FT	Region	797..798	
FT	FT	Modified-site	/label= autophosphorylation_sites	
FT	FT	Region	793	
FT	FT	Modified-site	/label= autophosphorylation_site	
FT	FT	Region	839..842	
FT	FT	Modified-site	/note= "putative"	
FT	FT	Region	839..842	
FT	FT	Modified-site	/label= binding_motif_for_pi3_kinase	
FT	FT	Region	/note= "binding motif for phosphatidylinositol 3' kinase"	
FT	FT	Region	827..827	
FT	FT	Modified-site	/label= potential_substrate_binding_site	
FT	FT	Region	506..509	
FT	FT	Modified-site	/label= putative_receptor_binding_site_for_SMC	

ID	AAW34674	standard; Protein; 563 AA.
XX	AAW34674;	
AC	17-FEB-1998	(first entry)
DT		
XX		
XX	Human mammary carcinoma kinase 10 (MCK-10) splice variant 2.	
XX		
KM	Mammary carcinoma kinase: MCK-10; receptor tyrosine kinase;	
KM	Proliferative disease; cancer; insulin receptor family;	
KM	Tyrosine kinase neurotrophin receptor; MCK-10 activity;	
KM	neurological disorder; aberrant expression.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..18
FT	Protein	/label= signal_sequence
FT		19..919
FT	Domain	/note= "mature_protein"
FT		31..185
FT	Cleavage-site	/label= Discoidin_I-like_domain
FT		304..307
FT	Region	/label= endopeptidase_furin
FT		/note= "putative precursor cleavage site"
FT		48..439
FT	Binding-site	/label= transmembrane_region
FT		617..627
FT	Modified-site	/label= ATP_binding_motif
FT		797..798
FT		/label= autophosphorylation_sites
FT		/note= "putative"
FT		793
FT	Modified-site	/label= autophosphorylation_site
FT		/note= "putative"
FT		839..842
FT	Binding-site	/label= binding_motif_for_pi3_kinase
FT		/note= "binding motif for phosphatidylinositol
FT		kinase"
FT		827..827
FT	Blinding-site	/label= potential_substrate_binding_site
FT		506..509
FT	Blinding-site	/label= putative_receptor_binding_site_for_SHC
FT		

CC adenocarcinoma RNA. The nt sequence of the novel receptor,
 CC designated CCK-2, is given in AA092521 and the deduced AA sequence in
 CC AAR75503. Analysis of the CCK-2 nt and AA sequence indicated
 CC significant homology of the CCK-10 throughout the extracellular,
 CC transmembrane and intracellular regions. The regions of homology
 CC extend into the N-terminus consensus sequence for the discoidin I
 CC like family of proteins.

XX Sequence 855 AA:

1 Query Match 48.8%; Score 2404; DB 16; Length 855;
 Best Local Similarity 51.8%; Pred. No. 5,7e-176;
 Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

OY 3 PEAISLLILLVAGSDAMKGFDPACRYALGMODRITPDSISASSWSSTAAHS 62
 DB 5 PMLILVILFILLPLIS---sakaqvnapalcrlypmsggqipdedltasqwsesatakyg 61
 OY 63 RLESSDGDGAWCPAGSVFPEKE-EEYLQVDLQRLHLVALVGTGGRHAGLGKESRSYRLR 121
 DB 62 RLDSEEGDGAWEPELPEVEDDLKEFIDQLHCHLHFTLVGTGRHAGNGLEFAPMYKLN 121
 OY 122 YSRDGRKMGKMDKMGQEVISGNEDEGVYLDLGPMAVRLRYEYPRADRVASVCLRYE 181
 DB 122 YSRDGRKMGKMDKMGQEVISGNEDEGVYLDLGPMAVRLRYEYPRADRVASVCLRYE 181
 OY 182 IYGCILMRGLLSTYAPVGTMTL--SEAVYLDSTYDGHVGTGGLGGLADGVYGLD 239
 DB 182 IYGCILMRGLLSTYAPVGTMTL--SEAVYLDSTYDGHVGTGGLGGLADGVYGLD 239
 OY 240 DEKRSQELVMPGVDYVGNHNSFSGYEMEFEDRLAFAQMOYHNNMHTLGARLGG 299
 DB 240 DEKRSQELVMPGVDYVGNHNSFSGYEMEFEDRLAFAQMOYHNNMHTLGARLGG 299
 OY 241 dltqchehyvwpgydyvgrnesatcngyleimfeatrlntumkvchmmfakgykltx 300
 DB 241 dltqchehyvwpgydyvgrnesatcngyleimfeatrlntumkvchmmfakgykltx 300
 OY 300 GVECFRRRGPANAMEGEPNRHNLGNTLGDPRARAVSVPLGGRVARELQCFLEFAGPMLLF 359
 DB 300 GVECFRRRGPANAMEGEPNRHNLGNTLGDPRARAVSVPLGGRVARELQCFLEFAGPMLLF 359
 OY 301 evqcyf-tseasewepnaistfplvldvnpasrfvtvphhmasaalkqyhtadcmmt 359
 DB 301 evqcyf-tseasewepnaistfplvldvnpasrfvtvphhmasaalkqyhtadcmmt 359
 OY 360 SPISITSD-VVNNSSPALGCTFPAPAWPPGPPPTFSSLELEPRQGVAKAEGSPYAI 418
 DB 360 SPISITSD-VVNNSSPALGCTFPAPAWPPGPPPTFSSLELEPRQGVAKAEGSPYAI 418
 OY 360 seiltqsdamynseal---ptsp-----naplytdpmlkvdadntrxi 400
 DB 360 seiltqsdamynseal---ptsp-----naplytdpmlkvdadntrxi 400
 OY 419 IIGCVAILLILLIITALLMRLHMRRLSKAERYLEELVHLSVPDITLNNR--P 476
 DB 419 IIGCVAILLILLIITALLMRLHMRRLSKAERYLEELVHLSVPDITLNNR--P 476
 OY 401 IIGCVAILLILLIITALLMRLHMRRLSKAERYLEELVHLSVPDITLNNR--P 476
 DB 401 IIGCVAILLILLIITALLMRLHMRRLSKAERYLEELVHLSVPDITLNNR--P 476
 OY 477 GPREP-----PPYQEPRRGNPNRPHSABCVPMGSALLLSNPAYRLILATYAR 523
 DB 477 GPREP-----PPYQEPRRGNPNRPHSABCVPMGSALLLSNPAYRLILATYAR 523
 OY 461 spsegsnstydrifrlprdygep-----srllrkllpef----- 494
 DB 461 spsegsnstydrifrlprdygep-----srllrkllpef----- 494
 OY 524 PRGPPPPPPAPAKPNTQAVSGDYDEPEKPGAPLPPPPQNSVPRHAEADIVYLGCVTGG 583
 DB 524 PRGPPPPPPAPAKPNTQAVSGDYDEPEKPGAPLPPPPQNSVPRHAEADIVYLGCVTGG 583
 OY 495 -----apgeesegscgvkvkpygpsp-----egvphyaedivlnlqvvtg 535
 DB 495 -----apgeesegscgvkvkpygpsp-----egvphyaedivlnlqvvtg 535
 OY 584 NTYAVPALPAGVADGPPRYV-DEPRSRRLRFRKELGSGGEGVHLGVDSPODLVSDPFL 642
 DB 584 NTYAVPALPAGVADGPPRYV-DEPRSRRLRFRKELGSGGEGVHLGVDSPODLVSDPFL 642
 OY 536 ntyrparvtmdlsgkdvaveefprklltfkxlgvqgvevhlcevegmefkddidai 595
 DB 536 ntyrparvtmdlsgkdvaveefprklltfkxlgvqgvevhlcevegmefkddidai 595
 OY 643 NVKRGHPLLVAVKILRPATKNASFLSFRNDELKEVKIMSRKDPNITRLGVCYQDDP 702
 DB 643 NVKRGHPLLVAVKILRPATKNASFLSFRNDELKEVKIMSRKDPNITRLGVCYQDDP 702
 OY 596 dvasanpylvavkmlradanaka-----rnfllkekikmsrlkdpnlhllsvcltdp 649
 DB 596 dvasanpylvavkmlradanaka-----rnfllkekikmsrlkdpnlhllsvcltdp 649
 OY 703 LCMITDYHENGDLNPLSHOLEDKAEGAPDGOAOGPTISYPMLLHVAAOIASGMRY 762
 DB 703 LCMITDYHENGDLNPLSHOLEDKAEGAPDGOAOGPTISYPMLLHVAAOIASGMRY 762
 OY 650 lcmileymengdlngflsh-----pnussssdvrtvsytlkikmacqiasgmly 700
 DB 650 lcmileymengdlngflsh-----pnussssdvrtvsytlkikmacqiasgmly 700
 OY 763 LATLNFVHDLATRNCLVCENFTIKIADGMSRNLYAGYVVOGRAVYPIRMMAECLT 822
 DB 763 LATLNFVHDLATRNCLVCENFTIKIADGMSRNLYAGYVVOGRAVYPIRMMAECLT 822
 OY 701 lsslnfvhndlstrnclvgknkllktdagmsrnllysgdyvrltqgavaplthmswesll 760
 DB 701 lsslnfvhndlstrnclvgknkllktdagmsrnllysgdyvrltqgavaplthmswesll 760
 OY 833 MGRFTASDVMAFGVTLWEVLMLCRAQPPGOLTDROVLENAGEFFRDOOROVYLSRPPAC 882
 DB 833 MGRFTASDVMAFGVTLWEVLMLCRAQPPGOLTDROVLENAGEFFRDOOROVYLSRPPAC 882

DB 761 lgtftasdvwaifgvrlweficqegpysqlsdegvientseftrdgrrtylpqpalc 820
 OY 883 PGLTYELMRCWRESEBQRPFSOLHRLAE 913
 DB 821 pdsaykmlmscwrrdtknpsfgehlhlllg 851

RESULT 11

AA75505
 ID AAR75505 standard; Protein; 855 AA.

AC AAR75505;

XX 26-NOV-1995 (first entry)

DE Human colonic adenocarcinoma kinase 2 (CCK-2).

XX Mammary carcinoma kinase 10; MCK-10; transmembrane receptor; CCK-2;
 KW receptor tyrosine kinase; colonic adenocarcinoma kinase 2.

OS Homo sapiens.

PN WO9514089-A.

XX 26-MAY-1995.

PF 16-NOV-1994; 94WO-EP03799.

XX 16-NOV-1993; 93US-0153397.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Alves FHE, Ullrich A;

DR WPI; 1995-224055/29.

XX N-PSDB; AA092523.

PT New nucleic acid encoding CCK-2 receptor tyrosine kinase - and
 PT derived vectors, transformed cells, proteins and antibodies, useful
 PT for diagnosis and treatment of proliferative and nervous system
 PT diseases and for screening modulators

PS Disclosure; Page 74-77; 115pp; English.

XX A member of the mammary carcinoma kinase 10 (MCK-10) receptor

CC tyrosine kinase family was identified using a PCR (with two

CC degenerate oligo primer pools based on conserved sequences of the

CC kinase domains of receptor tyrosine kinases) and cDNA prep. from

CC colonic adenocarcinoma RNA. The nt sequence of the novel receptor,

CC designated CCK-2, is given in AA092523 and the deduced AA sequence in

CC AAR75503. Analysis of CCK-2 nt and AA sequences indicated significant

CC homology with MCK-10 throughout the extracellular, transmembrane

CC and intracellular regions. The regions of homology extend into the

CC N-terminus consensus sequence for the discoidin I like family of

CC proteins. CCK-2 was predominantly found in all stromal cells

CC whereas MCK-10 expression was strongly confined to neoplastic

CC cells themselves. Between the two RTs, the juxtaposition region

CC is the region of most extensive sequence divergence.

XX Sequence 855 AA:

Query Match 48.8%; Score 2404; DB 16; Length 855;
 Best Local Similarity 51.8%; Pred. No. 5,7e-176;
 Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

OY 3 PEAISLLILLVAGSDAMKGFDPACRYALGMODRITPDSISASSWSSTAAHS 62
 DB 5 PMLILVILFILLPLIS---sakaqvnapalcrlypmsggqipdedltasqwsesatakyg 61
 OY 63 RLESSDGDGAWCPAGSVFPEKE-EEYLQVDLQRLHLVALVGTGGRHAGLGKESRSYRLR 121
 DB 62 RLDSEEGDGAWEPELPEVEDDLKEFIDQLHCHLHFTLVGTGRHAGNGLEFAPMYKLN 121
 OY 122 YSRDGRKMGKMDKMGQEVISGNEDEGVYLDLGPMAVRLRYEYPRADRVASVCLRYE 181
 DB 122 YSRDGRKMGKMDKMGQEVISGNEDEGVYLDLGPMAVRLRYEYPRADRVASVCLRYE 181
 OY 182 IYGCILMRGLLSTYAPVGTMTL--SEAVYLDSTYDGHVGTGGLGGLADGVYGLD 239
 DB 182 IYGCILMRGLLSTYAPVGTMTL--SEAVYLDSTYDGHVGTGGLGGLADGVYGLD 239
 OY 240 DEKRSQELVMPGVDYVGNHNSFSGYEMEFEDRLAFAQMOYHNNMHTLGARLGG 299
 DB 240 DEKRSQELVMPGVDYVGNHNSFSGYEMEFEDRLAFAQMOYHNNMHTLGARLGG 299
 OY 241 dltqchehyvwpgydyvgrnesatcngyleimfeatrlntumkvchmmfakgykltx 300
 DB 241 dltqchehyvwpgydyvgrnesatcngyleimfeatrlntumkvchmmfakgykltx 300
 OY 300 GVECFRRRGPANAMEGEPNRHNLGNTLGDPRARAVSVPLGGRVARELQCFLEFAGPMLLF 359
 DB 300 GVECFRRRGPANAMEGEPNRHNLGNTLGDPRARAVSVPLGGRVARELQCFLEFAGPMLLF 359
 OY 301 evqcyf-tseasewepnaistfplvldvnpasrfvtvphhmasaalkqyhtadcmmt 359
 DB 301 evqcyf-tseasewepnaistfplvldvnpasrfvtvphhmasaalkqyhtadcmmt 359
 OY 360 SPISITSD-VVNNSSPALGCTFPAPAWPPGPPPTFSSLELEPRQGVAKAEGSPYAI 418
 DB 360 SPISITSD-VVNNSSPALGCTFPAPAWPPGPPPTFSSLELEPRQGVAKAEGSPYAI 418
 OY 360 seiltqsdamynseal---ptsp-----naplytdpmlkvdadntrxi 400
 DB 360 seiltqsdamynseal---ptsp-----naplytdpmlkvdadntrxi 400
 OY 419 IIGCVAILLILLIITALLMRLHMRRLSKAERYLEELVHLSVPDITLNNR--P 476
 DB 419 IIGCVAILLILLIITALLMRLHMRRLSKAERYLEELVHLSVPDITLNNR--P 476
 OY 401 IIGCVAILLILLIITALLMRLHMRRLSKAERYLEELVHLSVPDITLNNR--P 476
 DB 401 IIGCVAILLILLIITALLMRLHMRRLSKAERYLEELVHLSVPDITLNNR--P 476
 OY 477 GPREP-----PPYQEPRRGNPNRPHSABCVPMGSALLLSNPAYRLILATYAR 523
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 OY 461 spsegsnstydrifrlprdygep-----srllrkllpef----- 494
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 OY 524 PRGPPPPPPAPAKPNTQAVSGDYDEPEKPGAPLPPPPQNSVPRHAEADIVYLGCVTGG 583
 DB 524 PRGPPPPPPAPAKPNTQAVSGDYDEPEKPGAPLPPPPQNSVPRHAEADIVYLGCVTGG 583
 OY 495 -----apgeesegscgvkvkpygpsp-----egvphyaedivlnlqvvtg 535
 DB 495 -----apgeesegscgvkvkpygpsp-----egvphyaedivlnlqvvtg 535
 OY 584 NTYAVPALPAGVADGPPRYV-DEPRSRRLRFRKELGSGGEGVHLGVDSPODLVSDPFL 642
 DB 584 NTYAVPALPAGVADGPPRYV-DEPRSRRLRFRKELGSGGEGVHLGVDSPODLVSDPFL 642
 OY 536 ntyrparvtmdlsgkdvaveefprklltfkxlgvqgvevhlcevegmefkddidai 595
 DB 536 ntyrparvtmdlsgkdvaveefprklltfkxlgvqgvevhlcevegmefkddidai 595
 OY 643 NVKRGHPLLVAVKILRPATKNASFLSFRNDELKEVKIMSRKDPNITRLGVCYQDDP 702
 DB 643 NVKRGHPLLVAVKILRPATKNASFLSFRNDELKEVKIMSRKDPNITRLGVCYQDDP 702
 OY 596 dvasanpylvavkmlradanaka-----rnfllkekikmsrlkdpnlhllsvcltdp 649
 DB 596 dvasanpylvavkmlradanaka-----rnfllkekikmsrlkdpnlhllsvcltdp 649
 OY 703 LCMITDYHENGDLNPLSHOLEDKAEGAPDGOAOGPTISYPMLLHVAAOIASGMRY 762
 DB 703 LCMITDYHENGDLNPLSHOLEDKAEGAPDGOAOGPTISYPMLLHVAAOIASGMRY 762
 OY 650 lcmileymengdlngflsh-----pnussssdvrtvsytlkikmacqiasgmly 700
 DB 650 lcmileymengdlngflsh-----pnussssdvrtvsytlkikmacqiasgmly 700
 OY 763 LATLNFVHDLATRNCLVCENFTIKIADGMSRNLYAGYVVOGRAVYPIRMMAECLT 822
 DB 763 LATLNFVHDLATRNCLVCENFTIKIADGMSRNLYAGYVVOGRAVYPIRMMAECLT 822
 OY 701 lsslnfvhndlstrnclvgknkllktdagmsrnllysgdyvrltqgavaplthmswesll 760
 DB 701 lsslnfvhndlstrnclvgknkllktdagmsrnllysgdyvrltqgavaplthmswesll 760
 OY 833 MGRFTASDVMAFGVTLWEVLMLCRAQPPGOLTDROVLENAGEFFRDOOROVYLSRPPAC 882
 DB 833 MGRFTASDVMAFGVTLWEVLMLCRAQPPGOLTDROVLENAGEFFRDOOROVYLSRPPAC 882

[illegible]

Key	Location/Qualifiers
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Modified-site	213
Modified-site	/note= "N-glycosylated"
Modified-site	261
Modified-site	/note= "N-glycosylated"
Modified-site	280
Modified-site	/note= "N-glycosylated"
Modified-site	328
Modified-site	/note= "N-glycosylated"
Modified-site	372
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Modified-site	503
Modified-site	/note= "putative autophosphorylation and substrate binding site"
Modified-site	736
Modified-site	/note= "putative autophosphorylation and substrate binding site"
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Modified-site	741
Modified-site	/note= "putative autophosphorylation and substrate binding site"
Modified-site	813
Modified-site	/note= "putative autophosphorylation and substrate binding site"
Modified-site	825
Modified-site	/note= "putative autophosphorylation and substrate binding site"
Modified-site	400..421
Modified-site	/label= "transmembrane-region"
Modified-site	/note= "putative"
Modified-site	30..185
Modified-site	/label= "DiscoIdin_1-like domain"
Modified-site	433..438
Modified-site	/label= "protein_kinase_C-binding_site"
Modified-site	/note= "putative"
Modified-site	US5677144-A.
Modified-site	14-OCT-1997.
Modified-site	08-NOV-1994;
Modified-site	94US-0336343.
Modified-site	16-NOV-1993;
Modified-site	93US-0153397.
Modified-site	(ALVE/) ALVES F H E.
Modified-site	(ULR/) ULRICH A.
Modified-site	Alves FHE, ULRICH A;
Modified-site	WPI: 1997-511869/47.
Modified-site	N-PDB: AAT93784.
Modified-site	Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding for it, useful for cancer diagnosis
Modified-site	Claim 5; Fig 3; 70pp; English.
Modified-site	The present sequence represents the amino acid sequence of human CCK-2, a member of the mammary carcinoma kinase 10 (MCK-10, AAM34672) family of receptor tyrosine kinases. The protein contains a remarkably high number of proline residues arranged as PXXP or PXXR repeats, suggesting a random coil structure for the hydrophilic juxtamembrane region. This region is probably a major domain for interactions with cellular substrates and other regulatory proteins. Expression of CCK-2 is associated with proliferative diseases such as cancer. The CCK-2 gene was identified by PCR and a cDNA prepared from colonic adenocarcinoma RNA. CCK-2 is expressed in a wide variety of cancer cell lines and tumour tissue. The CCK-2 nucleic acids can be used for diagnostic purposes to detect aberrant expression of CCK-2 genes. Engineered cell

CC lines, containing recombinant vectors with the present sequence, are
 CC useful for producing infectious retroviral particles. The cell lines may
 CC also be used to evaluate and screen drugs involved in CCR-2 activation
 CC and regulation.

XX
 XX Sequence 855 AA;

Query Match 48.8%; Score 2404; DB 19; Length 855;
 Best Local Similarity 51.8%; Pred. No. 5,7e-176;
 Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

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QY 3 PEALSSLLLLLVASGDADMKGHFDPKACRYALGMDRTIPDSISASSWSSTARRS 62
DB 5 pmlilvfillpils---sakeqvpaictcrlpmsggqldpeditassqwseslaakyg 61
QY 63 RLESSDGDGAWCPAGSVFPEK-EEYLQVDLQRLHLVALVGTGGRHAGLGKEFSRSYRLR 121
DB 62 rldseegdgawcpelprepddikefildhthlftlvtgtrhagghnfefapmykin 121
QY 122 YSRGRRMGMKDRWGQEVISGNEDEPGVYLKDLGPMVARYLRYPPRADRVASVCLAYE 181
DB 122 ysrgrtrwswrnthgkqyldgnanpydflkldleppivarfvrlpvtchsmvcmayve 181
QY 182 LYGLMARDGLSTYAPVGOMTYL--SEAVYLNDSTYDDHTVGGLOYGGLQADGVGGLD 239
DB 182 lygcwldglstysnapgqgfvlpjgsa1lylndsvdg-avgyamtegiyqldtgvsgld 240
QY 240 DFRKSQELRWPGYDYVGMNHSFSSGVEMEFEDRLRAFOAMQVHCNNMTLBARLPG 299
DB 241 dftqgheyhvwpdydvgnresatngyleimfedirinfctmknchmfmakvklrk 300
QY 300 GVECRFRGRPMAMGEGMRHNLGCLDPRARAVSVPLGGRVARELQCRFLFAGPWLIF 359
DB 301 evqcyf-rseasewepna1sflp1yldvnpaarfvtvplhmasa1kcyhfadctmmf 359
QY 360 SEISFISD-VVNSSPALGTFPPAPMWPPOPPPIFSSLEPPGQOPVAKABESPAI 418
DB 360 selfqsdgaanymseal---psp-----mapctygmklkvdsntrl 400
QY 419 LIGCLVALIILLLIITALLMRLMRRLSKAERVLEELVHLVSGDTILLNNR--P 476
DB 401 l1gclvali1f1l1a1l1v1l1wrgfwqmk1ekasr1mdentv1slpsds1mfm1ns 460
QY 477 GPRP-----PRYGPRRGNPNPHSAPCVNGSALLSNPAYRLLATYARP 523
DB 461 spseqgsnstydrllf1r1pdyqep-----srl1rkl1p1ef----- 494
QY 524 PRGPRPTPAMAKPTNTQAVSGDYMEPEKPGAPLLPPRQNSVPHYAEADIVTLQVYTG 583
DB 495 -----apgeegsgsvvkvqpsgp-----egvphyaead1vnl1qgv199 535
QY 584 NTYAVPALPAGVAGDGPPIV-DEFRSRLRERKELGEGQFGEVHCEVDSPODLVSLDFPL 642
DB 536 ntyavpavtmdl1sgkdvaavefprk1l1tfkex1geggfgevh1cevegmekf1dkda1 595
QY 643 NVKRGHPLAAVKTLRDAIKNASFSLSFRNDP1KEYKMSRLKDPNIRLLGYCVODDP 702
DB 596 dvaangv1vaavkmlradakna-----rndf1kex1msr1l1kdpn1l1h1l1svcl1ddp 649
QY 703 ICMITIDMENGDNLQFSAHQLEDKAEGAPGCGAAGPISYPMILHLVAQAQIASGMRY 762
DB 650 lcmiteymengdnlqf1sr1e-----ppms1ssdv1tvsy1n1k1fma1tq1a1sgm1y 700
QY 763 LATLNFVHRLAFLRNCILVGENFTIKADFGMSRNLVAGDYRVGGRVAVLPRMVAWACIL 822
DB 701 l1s1l1nf1h1r1l1a1f1l1r1nc1l1v1g1n1f1k1a1d1f1g1s1n1l1y1g1d1y1r1g1r1v1p1l1r1m1s1w1s1l1 760
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DB 761 l1g1f1t1a1s1d1v1w1a1r1g1v1t1l1m1e1v1l1m1c1r1a1p1q1l1d1e1q1v1e1n1a1g1f1e1f1r1d1q1g1v1y1p1j1p1a1c1 820
QY 883 PGLYELMLRCMSRESEQRPPFSQLHRLAE 913

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DB 821 pdsvylm1scwrt1cknps1qel1h1llg 851

RESULT 13

AAW77114 standard; Protein; 855 AA.

AAW77114;

16-NOV-1998 (first entry)

Disco1din domain receptor 2 protein.

Disco1din domain receptor; transformation; metastasis; collagen; ss;
 Cleidocranial dysplasia; Stickler syndrome; extracellular matrix; MMP-1.

Homo sapiens.

W09834954-A2.

13-AUG-1998.

05-FEB-1998; 98WO-CA00093.

06-FEB-1997; 97US-0041578.

(MOUN) MOUNT SINAI HOSPITAL CORP.

Pawson A, Vogel W;

WPI; 1998-447168/38.

DR N-PSDB; AAV48292.

Novel ligands of disco1din domain receptor tyrosine kinase,
 especially collagen - useful for treating e.g. metastasis,
 cleidocranial dysplasia or Stickler syndrome

Disclosure; Fig 22a; 115pp; English.

The disco1din domain receptor (DDR) can be used to identify and evaluate
 substances which affect DDR receptor tyrosine kinase signalling pathways
 in the cell. Compounds which modulate such signalling pathways can be
 used to alter transformation or metastasis in mammals, to treat
 conditions involving structural or functional deregulation of collagens,
 e.g. Cleidocranial dysplasia or Stickler syndrome, conditions requiring
 modulation of extracellular matrix synthesis, degradation or remodelling,
 or to treat conditions needing modulation of MMP-1 expression such as
 wound healing.

Sequence 855 AA;

Query Match 48.8%; Score 2404; DB 19; Length 855;
 Best Local Similarity 51.8%; Pred. No. 5,7e-176;
 Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

```

QY 3 PEALSSLLLLLVASGDADMKGHFDPKACRYALGMDRTIPDSISASSWSSTARRS 62
DB 5 pmlilvfillpils---sakeqvpaictcrlpmsggqldpeditassqwseslaakyg 61
QY 63 RLESSDGDGAWCPAGSVFPEK-EEYLQVDLQRLHLVALVGTGGRHAGLGKEFSRSYRLR 121
DB 62 rldseegdgawcpelprepddikefildhthlftlvtgtrhagghnfefapmykin 121
QY 122 YSRGRRMGMKDRWGQEVISGNEDEPGVYLKDLGPMVARYLRYPPRADRVASVCLAYE 181
DB 122 ysrgrtrwswrnthgkqyldgnanpydflkldleppivarfvrlpvtchsmvcmayve 181
QY 182 LYGLMARDGLSTYAPVGOMTYL--SEAVYLNDSTYDDHTVGGLOYGGLQADGVGGLD 239
DB 182 lygcwldglstysnapgqgfvlpjgsa1lylndsvdg-avgyamtegiyqldtgvsgld 240

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Db 655 eymengdingfisthepisscsda-----tvsyankkmatqiasgmkyissln 704
 QY 768 FVHRLAARNCLVGENFTIKIDFGMSRNLYAGDYRVQGAVALPIRMAMECILMGKPT 827
 Db 705 fvhrdlatrnclyvknlytkladfgmsrnlsgdyrlyqgravlplrmwsweslllgkft 764
 QY 828 TASDVMAFGVILMEVIMLCRAQPFQGLTDEQVLENAGEFFROGROYVLSRPPACPGILY 887
 Db 765 tasdvmafgyvlwefctfcqeqpsqsdqevlentgetftrdgrqlylpapalcpdsy 824
 QY 888 ELMLRCMSRESEORPPFSQHLRFIAE 913
 Db 825 klmiscwretkhrpsfgeihlillq 850
 RESULT 15
 AAM81409
 ID AAM81409 standard; Protein: 854 AA.
 XX
 AC AAM81409;
 XX
 DT 22-JAN-1999 (first entry)
 XX
 DE Receptor protein tyrosine kinase (PTK) subtype tyro-10.
 XX
 KW PTK; receptor; protein tyrosine kinase; recombinant; grafting;
 KM diagnosis; tumour; skin transplant; connective tissue; tyro-10.
 XX
 OS Rattus sp.
 XX
 PN US837448-A.
 XX
 PD 17-NOV-1998.
 XX
 PF 02-MAY-1994; 94US-0237401.
 XX
 PR 15-MAY-1992; 92US-0884486.
 PR 02-MAY-1994; 94US-0237401.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Lal CHC, Lemke GE;
 XX
 DR WPI, 1999-023436/02.
 DR N-PSDB; AAV65317.
 XX
 XX Nucleic acids encoding protein tyrosine kinase subtypes - for
 PT identification of new subtypes and treatment of diseases associated
 PT with the kinase
 PS
 PS Claim 10: Columns 53-58; 47pp; English.
 XX
 CC This represents a receptor protein tyrosine kinase (PTK) subtype
 CC tyro-10. The invention provides sequences AAV65308 to AAV65313, AAV65315,
 CC and AAV65317 to AAV65319 that encode proteins having a tyrosine kinase
 CC domain and a tissue expression pattern of a receptor PTK subtype selected
 CC from tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10,
 CC tyro-11, and tyro-12, respectively. The polynucleotides are useful for
 CC the detection of tyrosine kinase domain sequences and detection of tissue
 CC expression patterns of PTK subtypes. The cDNAs can also be injected into
 CC oocytes, the proteins expressed, and expression products screened for
 CC using antibodies against tyrosine kinase epitopes. These subtypes
 CC sequences can be used for the design of oligonucleotides, for use in
 CC amplification reactions to isolate other subtype sequences. These
 CC (receptor) PTKs. Recombinant vectors expressing the subtypes associated with
 CC into skin transplants, then grafting these into the connective tissue of
 CC the dermis, thus specifically targeting tumours as the proteins are
 CC released from the matrix.
 XX
 XX Sequence 854 AA:

Query Match 48.7%; Score 2402; DB 20; Length 854;
 Best Local Similarity 51.9%; Pred. No. 8e-176;
 Matches 481; Conservative 119; Mismatches 220; Indels 106; Gaps 16;
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 QY 69 GDGAMCPAGSVPEKE-EEYLVDLQRLHVALYVQGGHAGAGLGEFERSRYLRLRSRGR 127
 Db 68 gdaawceipvpddlketlqldlrlhlltlyvgtrnaggghletapmyltnysrfgs 127
 QY 128 RMWGWKDRWGOEYVIGSNEDEPESGVLLKDLAPPVAVRLVFFYPADRVMSVCLRELYGCLM 187
 Db 128 rtwswtrnrlgkqyldgnanpydvfkdllepvtarfvrllypvtahsmvcmrvellygcvw 187
 QY 188 RDGLLSTYAPVQIMYL--SEAVYLNDSITYDGHVVGGLQYGGGLADGVGLDFRRSQ 245
 Db 188 ldglysynapagqgfvfllp9sillyndasydg-avgymteglqgltdqvsqldfdtqth 246
 QY 246 ELRWVPGDYVGMNSHSFSGVYEMEFEDRLRAQAOVHNNHTGALRLPGVECRF 305
 Db 247 ehywvpydyvgywnesatngfelmfdtrlnltmkvchnmftakgyvklkevqcyf 306
 QY 306 RRGPMAMEGEPRMRHNLGNLDPPARAVSVPLGGRVAFLOCRFLFAGPMLTFSEISFI 365
 Db 307 rrsasewepctavfplldvnpaarfvtvplhmrmasalkcqhfdctmmfseitfq 365
 QY 366 SD--VYNNSPALGTFPPAPMPPGPPPTNFSSLELEPRGOQVPAKAGSPITALIGCL 423
 Db 366 sdaamyns-----galptsp-----maptydpmkxvdantflllgcl 405
 QY 424 VAILLLLLLLIATMLMRLHWRRLLSKARRVLEELTYHLSVPGDTLLNNR-----PEPR 479
 Db 406 valfillallavllwrfwtkmlkaskarlnldemtyvslpesssmfnnrsspsq 465
 QY 480 EP-----PPYQEPFRGRNPPHSAFCVNGSALLNSPVRLLATYARPPRPG 528
 Db 466 esnstydrflrplrdygp-----srllrlpct----- 494
 QY 529 PPTPAMAKPTNTQAYSQGYMEPEKFGAPLPPPPONSVPYHAADYVLTAGVTGANTYAV 588
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 QY 648 HPLVAVKILRPDATKNASFLSRNDPLKEVKMSRLKDNITRLGVCVQDDPLCMIT 707
 Db 601 qpvlyavvkmrlradankna-----rndllkkelkmsrltkpnlrltlavctteplcmllt 654
 QY 708 DYMEGNDINQFLSAHQLEDKAAEGAPGDGAAGPTISYPMILHVAQAQISGMRYLATLN 767
 Db 655 eymengdingfisthepisscsda-----tvsyankkmatqiasgmkyissln 704
 QY 768 FVHRLAARNCLVGENFTIKIDFGMSRNLYAGDYRVQGAVALPIRMAMECILMGKPT 827
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 Db 765 tasdvmafgyvlwefctfcqeqpsqsdqevlentgetftrdgrqlylpapalcpdsy 824
 QY 888 ELMLRCMSRESEORPPFSQHLRFIAE 913
 Db 825 klmiscwretkhrpsfgeihlillq 850

Mon Oct 7 15:50:44 2002

Job time: 261 sec

us-08-153-397a-2.rag
